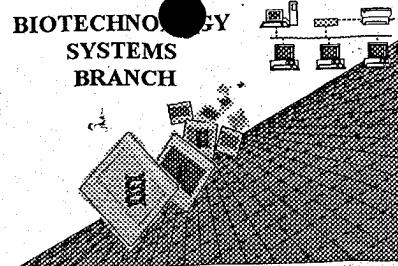


Forman

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/616,284

Source: 1600 RUSI

Date Processed by STIC: 8/6/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>
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SERIAL NUMBER: 09/6/6,284

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic Acid Sequences The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/616,284

DATE: 08/06/2001
TIME: 11:45:48

Input Set : A:\NEX77CP2.txt
Output Set: N:\CRF3\08062001\I616284.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Gold, Larry
4 Zichi, Dominic A.
5 Jenison, Robert D.
6 Schneider, Daniel J.
8 <120> TITLE OF INVENTION: Method and Apparatus for the Automated Generation of
9 Nucleic Acid Ligands
11 <130> FILE REFERENCE: NEX77/CIP2
13 <140> CURRENT APPLICATION NUMBER: 09/616,284
14 <141> CURRENT FILING DATE: 2000-07-14
16 <150> PRIOR APPLICATION NUMBER: 09/356,233
17 <151> PRIOR FILING DATE: 1999-07-16
19 <150> PRIOR APPLICATION NUMBER: 09/232,946
20 <151> PRIOR FILING DATE: 1999-01-19
22 <150> PRIOR APPLICATION NUMBER: 08/792,075
23 <151> PRIOR FILING DATE: 1997-01-31
25 <150> PRIOR APPLICATION NUMBER: 09/143,190
26 <151> PRIOR FILING DATE: 1998-08-27
28 <150> PRIOR APPLICATION NUMBER: 08/469,609
29 <151> PRIOR FILING DATE: 1995-06-06
31 <150> PRIOR APPLICATION NUMBER: 07/714,131
32 <151> PRIOR FILING DATE: 1991-06-10
34 <150> PRIOR APPLICATION NUMBER: 07/536,428
35 <151> PRIOR FILING DATE: 1990-06-11
37 <160> NUMBER OF SEQ ID NOS: 5
39 <170> SOFTWARE: PatentIn Ver. 2.0
41 <210> SEQ ID NO: 1
42 <211> LENGTH: 43
43 <212> TYPE: DNA
44 <213> ORGANISM: Artificial Sequence *see item 11 on Env Summary sheet*
46 <220> FEATURE:
47 <221> NAME/KEY: modified_base
48 <222> LOCATION: (1)..(43)
49 <223> OTHER INFORMATION: T at position 10 is substituted with DABCYL- (CH2)
50 6-; G at position 1 is substituted with 6-FAM.
52 <220> FEATURE: *duplicated*
53 <221> NAME/KEY: modified_base *above*
54 <222> LOCATION: (1)..(43)
55 <223> OTHER INFORMATION: T at position 10 is substituted with DABCYL- (CH2)
56 6-; G at position 1 is substituted with 6-FAM.
58 <400> SEQUENCE: 1
59 gagcgaagctctaatacgac tcactatagg gaggacgatg cgg 43
61 <210> SEQ ID NO: 2
62 <211> LENGTH: 51
63 <212> TYPE: DNA
64 <213> ORGANISM: Artificial Sequence *OK*
66 <220> FEATURE:
67 <221> NAME/KEY: modified_base

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/616,284

DATE: 08/06/2001
TIME: 11:45:48

Input Set : A:\NEX77CP2.txt
Output Set: N:\CRF3\08062001\I616284.raw

68 <222> LOCATION: (1)..(51)
69 <223> OTHER INFORMATION: T at position 10 is substituted with DABCYL- (CH2)
70 6-; G at position 1 is substituted with 6-FAM.
72 <220> FEATURE:
73 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
74 Sequence
76 <400> SEQUENCE: 2
77 gagcgaagct ctaatacgac tcactatagg gagacaagaa taaacgctca a 51
79 <210> SEQ ID NO: 3
80 <211> LENGTH: 61
81 <212> TYPE: DNA
82 <213> ORGANISM: Artificial Sequence
84 <220> FEATURE:
85 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
86 Sequence
88 <220> FEATURE:
89 <221> NAME/KEY: modified_base
90 <222> LOCATION: (1)..(61)
91 <223> OTHER INFORMATION: N at positions 16-45 is A, G, C or T.
93 <400> SEQUENCE: 3
94 gggaggacga tgccggnnnn nnnnnnnnnn nnnnnnnnnn nnnnncagac gacgagcggg 60
95 a 61
97 <210> SEQ ID NO: 4
98 <211> LENGTH: 23
99 <212> TYPE: DNA
100 <213> ORGANISM: Artificial Sequence
102 <220> FEATURE:
103 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
104 Sequence
106 <400> SEQUENCE: 4
107 atatatatgg gaggacgtcg cg 23
109 <210> SEQ ID NO: 5
110 <211> LENGTH: 24
111 <212> TYPE: DNA
112 <213> ORGANISM: Artificial Sequence
114 <220> FEATURE:
115 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
116 Sequence
118 <400> SEQUENCE: 5
119 tttttttttc ccgctcgtcg tctg 24

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/616,284

DATE: 08/06/2001
TIME: 11:45:49

Input Set : A:\NEX77CP2.txt
Output Set: N:\CRF3\08062001\I616284.raw

L:94 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3